> This Raw Listing contains the General Information
> Section and up to first 5 pages.

ENTERED

```
1    <110> APPLICANT: Oppmann, Birgit
2          Timans, Jacqueline C.
3          Kastelein, Robert A.
4          Bazan, J. Fernando
5    <120> TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods
6    <130> FILE REFERENCE: DX0935K
7    <140> CURRENT APPLICATION NUMBER: US/09/521,335
8    <141> CURRENT FILING DATE: 2000-03-09
9    <160> NUMBER OF SEQ ID NOS: 13
10   <170> SOFTWARE: PatentIn Ver. 2.0
11   <210> SEQ ID NO 1
12   <211> LENGTH: 1790
13   <212> TYPE: DNA
14   <213> ORGANISM: primate
15   <220> FEATURE:
16   <221> NAME/KEY: CDS
17   <222> LOCATION: (162)..(806)
18   <220> FEATURE:
19   <221> NAME/KEY: mat_peptide
20   <222> LOCATION: (213)..(806)
21   <400> SEQUENCE: 1
22         ccgagcgaaa aaaacctgcg agtgggcctg gcggatggga ttattaaagc ttcgccggag 60
23         ccgcggctcg ccctcccact ccgccagcct ccgggagagg agccgcaccc ggccggcccg 120
24         gccccagccc catggacctc cgagcagggg actcgtgggg g atg tta gcg tgc ctg 176
25                                                     Met Leu Ala Cys Leu
26                                                             -15
27         tgc acg gtg ctc tgg cac ctc cct gca gtg cca gct ctc aat cgc aca    224
28         Cys Thr Val Leu Trp His Leu Pro Ala Val Pro Ala Leu Asn Arg Thr
29              -10              -5              -1  1
30         ggg gac cca ggg cct ggc ccc tcc atc cag aaa acc tat gac ctc acc    272
31         Gly Asp Pro Gly Pro Gly Pro Ser Ile Gln Lys Thr Tyr Asp Leu Thr
32          5              10              15              20
33         cgc tac ctg gag cac caa ctc cgc agc ttg gct ggg acc tat ctg aac    320
34         Arg Tyr Leu Glu His Gln Leu Arg Ser Leu Ala Gly Thr Tyr Leu Asn
35                          25              30              35
36         tac ctg ggc ccc cct ttc aac gag cca gac ttc aac cct ccc cgc ctg    368
37         Tyr Leu Gly Pro Pro Phe Asn Glu Pro Asp Phe Asn Pro Pro Arg Leu
38                      40              45              50
39         ggg gca gag act ctg ccc agg gcc act gtt gac ttg gag gtg tgg cga    416
40         Gly Ala Glu Thr Leu Pro Arg Ala Thr Val Asp Leu Glu Val Trp Arg
41                      55              60              65
42         agc ctc aat gac aaa ctg cgg ctg acc cag aac tac gag gcc tac agc    464
43         Ser Leu Asn Asp Lys Leu Arg Leu Thr Gln Asn Tyr Glu Ala Tyr Ser
44              70              75              80
```

```
45        cac ctt ctg tgt tac ttg cgt ggc ctc aac cgt cag gct gcc act gct    512
46        His Leu Leu Cys Tyr Leu Arg Gly Leu Asn Arg Gln Ala Ala Thr Ala
47          85                    90                  95                 100
48        gag ctg cgc cgc agc ctg gcc cac ttc tgc acc agc ctc cag ggc ctg    560
49        Glu Leu Arg Arg Ser Leu Ala His Phe Cys Thr Ser Leu Gln Gly Leu
50                         105                 110                 115
51        ctg ggc agc att gcg ggc gtc atg gca gct ctg ggc tac cca ctg ccc    608
52        Leu Gly Ser Ile Ala Gly Val Met Ala Ala Leu Gly Tyr Pro Leu Pro
53                         120                 125                 130
54        cag ccg ctg cct ggg act gaa ccc act tgg act cct ggc cct gcc cac    656
55        Gln Pro Leu Pro Gly Thr Glu Pro Thr Trp Thr Pro Gly Pro Ala His
56                         135                 140                 145
57        agt gac ttc ctc cag aag atg gac gac ttc tgg ctg ctg aag gag ctg    704
58        Ser Asp Phe Leu Gln Lys Met Asp Asp Phe Trp Leu Leu Lys Glu Leu
59            150                 155                 160
60        cag acc tgg ctg tgg cgc tcg gcc aag gac ttc aac cgg ctc aag aag    752
61        Gln Thr Trp Leu Trp Arg Ser Ala Lys Asp Phe Asn Arg Leu Lys Lys
62        165                 170                 175                 180
63        aag atg cag cct cca gca gct gca gtc acc ctg cac ctg ggg gct cat    800
64        Lys Met Gln Pro Pro Ala Ala Ala Val Thr Leu His Leu Gly Ala His
65                         185                 190                 195
66        ggc ttc tgacttctga ccttctcctc ttcgctcccc cttcaaaccc tgctcccact    856
67        Gly Phe
```

W-->   68

```
69        ttgtgagagc cagccctgta tgccaacacc tgttgagcca ggagacagaa gctgtgagcc 916
70        tctggccctt tcctggaccg gctgggcgtg tgatgcgatc agccctgtct cctccccacc 976
71        tcccaaaggt ctaccgagct ggggaggagg tacagtaggc cctgtcctgt cctgtttcta 1036
72        caggaagtca tgctcgaggg agtgtgaagt ggttcaggtt ggtgcagagg cgctcatggc 1096
73        ctcctgcttc ttgcctacca cttggccagt gcccacccag cccctcaggt ggcacatctg 1156
74        gagggcaggg gttgaggggc caccaccaca catgcctttc tggggtgaag ccctttggct 1216
75        gccccactct ccttggatgg gtgttgctcc cttatcccca aatcactcta tacatccaat 1276
76        tcaggaaaca aacatggtgg caattctaca caaaaagaga tgagattaac agtgcagggt 1336
77        tggggtctgc attggaggtg ccctataaac cagaagagaa aatactgaaa gcacaggggc 1396
78        agggacagac cagaccagac ccaggagtct ccaaagcaca gagtggcaaa caaaacccga 1456
79        gctgagcatc aggaccttgc ctcgaattgt cttccagtat tacggtgcct cttctctgcc 1516
80        cccttttccca gggtatctgt gggttgccag gctggggagg gcaaccatag ccacaccaca 1576
81        ggatttcctg aaagtttaca atgcagtagc attttggggt gtaggtggc agctcccaa  1636
82        ggccctgccc cccagccca cccactcatg actctaagtg tgttgtatta atattatttt 1696
83        atttggagat gttatttatt agatgatatt tattgcagaa tttctattct tgtattaaca 1756
84        aataaaatgc ttgccccaga acaaaaaaaa aaaa                              1790
```

85   <210> SEQ ID NO 2
86   <211> LENGTH: 215
87   <212> TYPE: PRT
88   <213> ORGANISM: primate
89   <400> SEQUENCE: 2

```
90        Met Leu Ala Cys Leu Cys Thr Val Leu Trp His Leu Pro Ala Val Pro
91                     -15                 -10                 -5
92        Ala Leu Asn Arg Thr Gly Asp Pro Gly Pro Gly Pro Ser Ile Gln Lys
93         -1   1                  5                  10                 15
94        Thr Tyr Asp Leu Thr Arg Tyr Leu Glu His Gln Leu Arg Ser Leu Ala
```

```
 95                         20                      25                       30
 96          Gly Thr Tyr Leu Asn Tyr Leu Gly Pro Pro Phe Asn Glu Pro Asp Phe
 97                     35                      40                      45
 98          Asn Pro Pro Arg Leu Gly Ala Glu Thr Leu Pro Arg Ala Thr Val Asp
 99                 50                      55                      60
100          Leu Glu Val Trp Arg Ser Leu Asn Asp Lys Leu Arg Leu Thr Gln Asn
101             65                      70                      75
102          Tyr Glu Ala Tyr Ser His Leu Leu Cys Tyr Leu Arg Gly Leu Asn Arg
103             80                      85                      90                      95
104          Gln Ala Ala Thr Ala Glu Leu Arg Arg Ser Leu Ala His Phe Cys Thr
105                     100                     105                     110
106          Ser Leu Gln Gly Leu Leu Gly Ser Ile Ala Gly Val Met Ala Ala Leu
107                     115                     120                     125
108          Gly Tyr Pro Leu Pro Gln Pro Leu Pro Gly Thr Glu Pro Thr Trp Thr
109                 130                     135                     140
110          Pro Gly Pro Ala His Ser Asp Phe Leu Gln Lys Met Asp Asp Phe Trp
111             145                     150                     155
112          Leu Leu Lys Glu Leu Gln Thr Trp Leu Trp Arg Ser Ala Lys Asp Phe
113          160                     165                     170                     175
114          Asn Arg Leu Lys Lys Lys Met Gln Pro Pro Ala Ala Ala Val Thr Leu
115                     180                     185                     190
116          His Leu Gly Ala His Gly Phe
117                     195
118   <210> SEQ ID NO 3
119   <211> LENGTH: 648
120   <212> TYPE: DNA
121   <213> ORGANISM: primate
122   <220> FEATURE:
123   <221> NAME/KEY: CDS
124   <222> LOCATION: (1)..(645)
125   <220> FEATURE:
126   <221> NAME/KEY: mat_peptide
127   <222> LOCATION: (52)..(645)
128   <400> SEQUENCE: 3
129          atg tta gct tgc cta tgc acg gtg ctg tgg cac ctc cct gca gtg cca      48
130          Met Leu Ala Cys Leu Cys Thr Val Leu Trp His Leu Pro Ala Val Pro
131                 -15                     -10                      -5
132          gct ctt aat cgc aca gga gat cca ggc cct ggc ccc tcc atc cag aaa      96
133          Ala Leu Asn Arg Thr Gly Asp Pro Gly Pro Gly Pro Ser Ile Gln Lys
134          -1   1               5                       10                      15
135          acc tat gac ctc acc cgc tac ctg gag cat caa ctc cgc agc tta gct     144
136          Thr Tyr Asp Leu Thr Arg Tyr Leu Glu His Gln Leu Arg Ser Leu Ala
137                     20                      25                      30
138          ggg acc tac ctg aac tac ctg ggg ccc cct ttc aac gag cct gac ttc     192
139          Gly Thr Tyr Leu Asn Tyr Leu Gly Pro Pro Phe Asn Glu Pro Asp Phe
140                     35                      40                      45
141          aat cct cct cga ctg ggg gca gaa act ctg ccc agg gcc acg gtc aac     240
142          Asn Pro Pro Arg Leu Gly Ala Glu Thr Leu Pro Arg Ala Thr Val Asn
143                 50                      55                      60
144          ttg gaa gtg tgg cga agc ctc aat gac agg ctg cgg ctg acc cag aac     288
```

```
145        Leu Glu Val Trp Arg Ser Leu Asn Asp Arg Leu Arg Leu Thr Gln Asn
146             65                  70                  75
147        tat gag gcg tac agt cac ctc ctg tgt tac ttg cgt ggc ctc aac cgt    336
148        Tyr Glu Ala Tyr Ser His Leu Leu Cys Tyr Leu Arg Gly Leu Asn Arg
149             80                  85                  90                  95
150        cag gct gcc aca gct gaa ctc cga cgt agc ctg gcc cac ttc tgt acc    384
151        Gln Ala Ala Thr Ala Glu Leu Arg Arg Ser Leu Ala His Phe Cys Thr
152                            100                 105                 110
153        agc ctc cag ggc ctg ctg ggc agc att gca ggt gtc atg gcg acg ctt    432
154        Ser Leu Gln Gly Leu Leu Gly Ser Ile Ala Gly Val Met Ala Thr Leu
155                            115                 120                 125
156        ggc tac cca ctg ccc cag cct ctg cca ggg act gag cca gcc tgg gcc    480
157        Gly Tyr Pro Leu Pro Gln Pro Leu Pro Gly Thr Glu Pro Ala Trp Ala
158                            130                 135                 140
159        cct ggc cct gcc cac agt gac ttc ctc cag aag atg gat gac ttc tgg    528
160        Pro Gly Pro Ala His Ser Asp Phe Leu Gln Lys Met Asp Asp Phe Trp
161             145                 150                 155
162        ctg ctg aag gag ctg cag acc tgg cta tgg cgt tca gcc aag gac ttc    576
163        Leu Leu Lys Glu Leu Gln Thr Trp Leu Trp Arg Ser Ala Lys Asp Phe
164             160                 165                 170                 175
165        aac cgg ctt aag aag aag atg cag cct cca gca gct tca gtc acc ctg    624
166        Asn Arg Leu Lys Lys Lys Met Gln Pro Pro Ala Ala Ser Val Thr Leu
167                            180                 185                 190
168        cac ttg gag gcc cat ggt ttc tga                                    648
169        His Leu Glu Ala His Gly Phe
170                            195
171   <210> SEQ ID NO 4
172   <211> LENGTH: 215
173   <212> TYPE: PRT
174   <213> ORGANISM: primate
175   <400> SEQUENCE: 4
176        Met Leu Ala Cys Leu Cys Thr Val Leu Trp His Leu Pro Ala Val Pro
177                 -15                 -10                 -5
178        Ala Leu Asn Arg Thr Gly Asp Pro Gly Pro Gly Pro Ser Ile Gln Lys
179        -1   1                  5                  10                  15
180        Thr Tyr Asp Leu Thr Arg Tyr Leu Glu His Gln Leu Arg Ser Leu Ala
181                            20                  25                  30
182        Gly Thr Tyr Leu Asn Tyr Leu Gly Pro Pro Phe Asn Glu Pro Asp Phe
183                            35                  40                  45
184        Asn Pro Pro Arg Leu Gly Ala Glu Thr Leu Pro Arg Ala Thr Val Asn
185                            50                  55                  60
186        Leu Glu Val Trp Arg Ser Leu Asn Asp Arg Leu Arg Leu Thr Gln Asn
187             65                  70                  75
188        Tyr Glu Ala Tyr Ser His Leu Leu Cys Tyr Leu Arg Gly Leu Asn Arg
189             80                  85                  90                  95
190        Gln Ala Ala Thr Ala Glu Leu Arg Arg Ser Leu Ala His Phe Cys Thr
191                            100                 105                 110
192        Ser Leu Gln Gly Leu Leu Gly Ser Ile Ala Gly Val Met Ala Thr Leu
193                            115                 120                 125
194        Gly Tyr Pro Leu Pro Gln Pro Leu Pro Gly Thr Glu Pro Ala Trp Ala
```

```
  195                    130                  135                    140
  196          Pro Gly Pro Ala His Ser Asp Phe Leu Gln Lys Met Asp Asp Phe Trp
  197              145                  150                  155
  198          Leu Leu Lys Glu Leu Gln Thr Trp Leu Trp Arg Ser Ala Lys Asp Phe
  199          160                  165                  170                  175
  200          Asn Arg Leu Lys Lys Lys Met Gln Pro Pro Ala Ala Ser Val Thr Leu
  201                    180                  185                    190
  202          His Leu Glu Ala His Gly Phe
  203                    195
  204  <210> SEQ ID NO 5
  205  <211> LENGTH: 203
  206  <212> TYPE: PRT
  207  <213> ORGANISM: rodent
  208  <400> SEQUENCE: 5
  209          Met Lys Val Leu Ala Ala Gly Ile Val Pro Leu Leu Leu Leu Val Leu
  210            1               5                  10                  15
  211          His Trp Lys His Gly Ala Gly Ser Pro Leu Pro Ile Thr Pro Val Asn
  212                    20                  25                  30
  213          Ala Thr Cys Ala Ile Arg His Pro Cys His Gly Asn Leu Met Asn Gln
  214                    35                  40                  45
  215          Ile Lys Asn Gln Leu Ala Gln Leu Asn Gly Ser Ala Asn Ala Leu Phe
  216            50                  55                  60
  217          Ile Ser Tyr Tyr Thr Ala Gln Gly Glu Pro Phe Pro Asn Asn Val Glu
  218          65                  70                  75                  80
  219          Lys Leu Cys Ala Pro Asn Met Thr Asp Phe Pro Ser Phe His Gly Asn
  220                    85                  90                  95
  221          Gly Thr Glu Lys Thr Lys Leu Val Glu Leu Tyr Arg Met Val Ala Tyr
  222                    100                  105                  110
  223          Leu Ser Ala Ser Leu Thr Asn Ile Thr Arg Asp Gln Lys Val Leu Asn
  224                    115                  120                  125
  225          Pro Thr Ala Val Ser Leu Gln Val Lys Leu Asn Ala Thr Ile Asp Val
  226                    130                  135                  140
  227          Met Arg Gly Leu Leu Ser Asn Val Leu Cys Arg Leu Cys Asn Lys Tyr
  228          145                  150                  155                  160
  229          Arg Val Gly His Val Asp Val Pro Pro Val Pro Asp His Ser Asp Lys
  230                    165                  170                  175
  231          Glu Ala Phe Gln Arg Lys Lys Leu Gly Cys Gln Leu Leu Gly Thr Tyr
  232                    180                  185                  190
  233          Lys Gln Val Ile Ser Val Val Val Gln Ala Phe
  234                    195                  200
  235  <210> SEQ ID NO 6
  236  <211> LENGTH: 202
  237  <212> TYPE: PRT
  238  <213> ORGANISM: primate
  239  <400> SEQUENCE: 6
  240          Met Lys Val Leu Ala Ala Gly Val Val Pro Leu Leu Leu Val Leu His
  241            1               5                  10                  15
  242          Trp Lys His Gly Ala Gly Ser Pro Leu Pro Ile Thr Pro Val Asn Ala
  243                    20                  25                  30
  244          Thr Cys Ala Ile Arg His Pro Cys His Asn Asn Leu Met Asn Gln Ile
```

Line ? Error/Warning   Original Text
----- - --------------------------------------- ---------------------------------------
   68 W Invalid/Missing Amino Acid Numbering